•2"

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                earched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                   SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_votent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi:
15: sp_archeap:*
17: sp_archeap:*
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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461.889 Million cell updates/sec
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964
  MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184
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sp_phage:*
sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
   175
217
842
1193
938
1998
327
314
2233
595
1299
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485
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10
10
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10
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 Q974WB
Q971XB
Q971XB
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Q971XB
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Q97491
Q94711
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Q8vev6 mus musculu
Q94711 paramecium
Q94711 parabidopsis
O01892 caenorhabdi
O81820 arabidopsis
Q26489 spodoptera
Q8vfw0 mus musculu
Q9h677 homo sapien
Q8r221 mus musculu
                                                                                                    Q8r4w8 mus musculu
Q97d61 clostridium
Q8r566 mus musculu
Q9y1x8 ephydatia f
Q8rwY7 arabidopsis
Q9str8 arabidopsis
Q97491 ovis aries
                                                                                                                                                                                              Description
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	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	72.5	72.5	72.5	73	73	73	73	73.5	73.5	73.5	74	74	74.5	74.5	75	75	75	75.5	76	76	76.5	76.5	76.5	77	77	77.5	77.5	77.5	77.5
	7.5	7.5	7.5	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.9	7.9					8.0	•			8.0
	408	375	243	733	679	462	304	853	634	307	789	377	966	853	718	706	450	454	1805	748	1404	656	357	539	522	968	853	738	738
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٠	Q9ZQR4	Q22095	085853	Q9LMP0	Q9ZWD7	OMMISO 0	Q99UY7	Q40096	Q8T259	Q97RG2	Q91000	Q9RHU5	Q22378	Q9YKV7	Q9BI07	Q8T206	Q97E85	Q8T1T4	Q63661	042637	045251	Q9FJE3	Q9XV87	Q9X0N0	Q9M3B3	004623	Q9YKU7	081819	Q9LMN6
	Q9zqr4 arabidopsis	Q22095 caenorhabdi	Ø		Q9zwd7 arabidopsis	_	Q99uy7 staphylococ	Q40096 ipomoea tri	Q.	Q97rg2 streptococc	Q91000 gallus gall	Q9rhu5 streptomyce	Q22378 caenorhabdi	Q9ykv7 human immun	Q9bi07 entamoeba h	Q8t206 dictyosteli	Q97e85 clostridium	u	Q63661 rattus norv	042637 neurospora	O45251 caenorhabdi	Q9fje3 arabidopsis	Q9xv87 caenorhabdi	Q9x0n0 thermotoga	. Q9m3b3 arabidopsis	O04623 arabidopsis	Q9yku7 human immun	O81819 arabidopsis	Q91mn6 arabidopsis

## ALIGNMENTS

	ş 8	Дb	Ş	Дb	δ	Qu Be Ma	ŞQ	DR	RL	RT	RT	RA	R.P.	RN CX	200	ကို	SO	DE	D.	D, C	A A	RESULT Q8R4W8 ID Q	
130FIIASAFIWEEUN-EUAUSAHENNSVEVEALBUGSIBHVIINI 1/0	EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT	81 GLILALTLVGLVSWRWRQOLRTASPDTSEGVQQESLENVFVPSSET 129	57 WTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111	21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80	7 QCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAIL 56	Query Match 12.1%; Score 116.5; DB 11; Length 175; Best Local Similarity 29.4%; Pred. No. 0.0002; Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;	SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;	0257; AAL83914.1;	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.		"Identification of novel TRAPS binding protein, T3BP, which increases	Mizuno K., Irie S., Sato TA.:	SECURICE FROM N.A.	(1) NCBI_TaxID=10090;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Chordata; Craniata; Vertebrata;	Mus musculus (Mouse).	ng protein.	(TrEMBLrel. 21.	(TrEMBLrel: 21,	; -2002 (TYEMBITE)	LT 1 W8 Q8R4W8 PRELIMINARY; PRT; 175 AA.	

RESULT 2

Best Local Similarity

22.7%;

1.9;

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QBROSG
ID QBRO
AC QBRO
AC QBRO
DT 01-J
DT 01-J
DT 01-J
DT 01-J
DT 01-J
CC MAMM
OX NCB:
RN (1)
RP SEQI
RC TIS:
RA SETS:
RA SEX:
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Best Local Similarity
Matches 55; Conserv
     Query Match
                                              EMBL, BC02828
Hypothetical
SEQUENCE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8R056;
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AE007858; AAK81542.1; -.
InterPro; IPR000515; BPD transp.
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                              Strausberg R.;
Submitted (APR-2002) to the
EMBL, BC028286; AAH28286.1;
                                                                                                                                                                                                                                                                                                                           Hypothetical 94.5 kDa protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001
01-OCT-2001
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00528; BPD transp; 1.
PROSITE; PS00402; BPD TRANSP INN MEMBR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 824 /
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                              SSUE=EYE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 PLLLQLYVYYYGLPFLSDKLTMTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGQFEASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
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                                                   al protein.
842 AA; 5
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llarity 24.8%;
Conservative 2
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                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23743 MW; 36738BCDC0DE8A2F CRC64;
                                                   94478 MW;
     9.0%
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Last sequence update)
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5; Mismatches
Score
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Pred. No. 0
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Sciurognathi; Muridae; Murinae; Mus.
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  86.5;
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  Length
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  842;
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RESULT 4
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Q9Y1X8;
01-NOV-1999
         PROSITE;
PROSITE;
PROSITE;
PROSITE;
Kinase.
                                                                                                                                                                                                                                                                          Suga H., Katoh K., Miyara 1.; Sponge homologs of vertebrate protein tyrosine kinases and "Sponge homologs in the early evolution of animals before t
                                                                  ProDom; PD000001; Euk pkir
SMART; SM00261; FU; 6.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                              InterPro; IPR001245; Tyr_kinase.
Pfam; PF000757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99246375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Porifera,
Haplosclerida, Spongillidae, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                               the parazoan-eumetazoan split demonstrated tyrosine kinases from sponge and hydra.";
                                                                                                                                                                                                                                                                                                                                                                                                  Miyata T.
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                                                                                                                                                                                                                                    HSSP; P08631; 1AD5
                                                                                                                                                                                                                                              EMBL; AB006570;
                                                                                                                                                                                                                                                          3ene 280:195-201(2001
                                                                                                                                                                                                                                                                       parazoan-eumetazoan split.";
                                                                                                                                                                                                                                                                                                                   MEDLINE=21601119; PubMed=11738833;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=31330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydatia fluviatilis.
                                                                                                                                                                                      InterPro;
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                   PS00107; PROTEIN KINASE ATP; 1.
PS50011; PROTEIN KINASE DOM; 1.
PS00109; PROTEIN KINASE TYR; 1.
PS00652; TNFR_NGFR_1; UNKNOWN_1.
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
IPR002290; Ser thr pkinas
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IPR001368; TNFR_c6.
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AA;
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                                                                                          Euk_pkinase;
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M., Hoshiyama D.,
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Q8RWV7;
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 93
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Pred. No. 3.
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Best Local S
Matches 37
Takagi M., Takahashi H., Kabey "Cloning of sheep fas antigen! Submitted (MAR-1998) to the EMEL; AB011671; BAA37093.1; -- HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=LYMPHOCYTE;
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Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
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InterPro; IPR001368; TNFR_c6
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                                                                                                                                                                                                                           Kabeya H.,
tigen!";
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Ovis aries (Sheep).

Ovis aries (Sheep).

Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
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Choisne N., Robert C., Brottier P., Wincker P., Cattolic Choisne N., Robert M., Weissenbach J., Mewes H.W., I Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., I Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 1998 AA; 223513 MW; BB3D6A03CD248F55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation updat
EMBL/GenBank/DDBJ
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Pred. No. 11
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                                                Ohashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              327
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                                                Sugimoto C.,
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3 H.W., Rudd &
                                                                                                                                                                                                           Pecora; Bovoidea;
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RESULT
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Best Local
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Q8VEV6;
Q1-MAR-2002 (TrEMBLrel. 20, Cre
Q1-MAR-2002 (TrEMBLrel. 21, Lag
Q1-JUN-2002 (TrEMBLrel. 21, Lag
Q1-JUN-2002 (TrEMBLrel. 21, Lag
Q1-JUN-2003 (TrEMBLrel. 21, Lag
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Q1-JUN-2003 (TrEMBLrel. 21, Lag
Q1-JUN-2003 (TrEMBLrel. 21, Lag
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            Q94711;
Q94711;
01-FEB-1997
01-FEB-1997
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51C surface
                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AY073792; AAL61455.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOW
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang X., Firestein S.J.; "The olfactory receptor gene wat. Neurosci. 0:0-0(2002).
  Paramecium
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                   CLG-LSLIISLAVFVLMF---LLRKISSEPLKDEFKNTGSGLL
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97 (TrEMBLrel.
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ce protein.
m tetraurelia.
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Rodentia;
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                                                   Created)
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Pred. No.
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Pred. No. 2
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                  EMBL; L04999; AAA32844.1; -...
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF Ca.
InterPro; IPR000719; Euk_pkinase.
Pfam; PF00069; pkinase; I.

ProDom; PD000001; Euk pkinase; 1.

SMART; SM000179; EGF CA; 1.

SMART; SM00001; EGF Like; 1.

SMART; SM00001; EGF Like; 1.

PROSITE; PS01186; EGF Z; UNKNOWN 1.

PROSITE; PS01187; EGF Z; UNKNOWN 1.

PROSITE; PS01187; EGF Z; UNKNOWN 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Serine/threonine-protein kinase; Transferase.
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Q39191, 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR 2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nielsen E., You Y., Forney J.;
"Cysteine residue periodicity is a conserved structural feature variable surface proteins from Paramecium tetraurelia.";
J. Mol. Biol. 222:835-841(1991).
EMBL; M65164; AAA61740.1;
InterPro; IPR002895; Paramecium SA.
Pfam; PF01508; Paramecium SA; 25.
SEQUENCE 2233 AA; 237078 MW; C064FE0AF7BB873B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An Arabidopsis serine threonine kinase homologue with selected in yeast for its specificity for a thylakoid o
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MEDLINE=92106337; PubMed=1762150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93066369; PubMed=1438303;
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                                                                                                                                                                                                                                                                                                       InterPro; IPR002290; Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTVELCEAYKPSSNCV---PNGTKKGCMELAAKCESRTIKEQCDVAGTKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI-----LVTTKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d. Sci. U.S.A. 89:10989-10992(1992)
BELONGS TO THE SER/THR FAMILY OF P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                  thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 81.5; Di
%; Pred. No. 20;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
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                                         Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ____D
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SS

SEQUENCE

595

AA;

65899 MW;

Matches

39; œ

Local

Similarity

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Waterston R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ |
EMBL; AF003385; AAB54249.1; -.
HSSP; P05164; ICXP.
InterPro; IPR002007; Anim_peroxidase.
Pfam; PF03098; An_peroxidase; 1.
SEQUENCE 773 AA; 83992 MW; 4E3373FDA4EC67(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of C. elegans Submitted (MAY-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode investigating biology. The C. elections 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-JUN-2002 (TrEMBLrel. 21,
   SSLNCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ
                                    EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA----TE
                                                                           IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG
                                                                                                              IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV
                                                                                                                                                   PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
                                                                                                                                                                                     PCQLRCSSNTPPLTCQ------RYCN----ASVTNSVKGTNAILWTCL---GLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLSGPSNVDVKIFTEDGMKKATNGYAESRÍLGQGGQGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GMANID-----LEKSRTG--DEILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMSCKRKEFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRCNEGFDGNPYLSAGCQDVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR-----YCNA-----SV
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%;
                                                                                                                                                                                                                          8.4%; Score 81; DB
21.7%; Pred. No. 6.6;
tive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid R08F11.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans
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                                                                                                                                                                                                                                                                                                  4E3373FDA4EC67C7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. elegans: a platform for egans Sequencing Consortium.";
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                                                                                                                                                                                                                                            6.6;
                                                                                                                                                                                                                                                             DB 5; Length 773,
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                                                                                                                                                                                                                        91;
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                                      176
                                                                           303
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                                                                                                                                                   Matches
                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriumi, M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Finnozaki K., Davis R.W., Ecker J.R., Theologis A., Full Length CDNA of gene F16F4.6 (GI:8920634) ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Wall-associated kinase 1 (Putative wall-associated
WAKI OR F16F4.6.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     081820
081820;
                                                                                                                                                                                                               PROSITE; PROTEIN KINASE DOM; 1.

PROSITE; PSO011, PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Serine/chreonine-protein kinase; Transferase.

Repeat; Serine/chreonine-protein kinase; Transferase.

SEQUENCE 735 AA; 81211 MW; AAD41A28296093E6 CRC64;
                                                                                                                                                                                                                                                                         PROSITE; PS00010; ASX_HYDROXYL; UPROSITE; PS01186; EGF 2; UNKNOWN PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00111; PROTEIN KINASE PROSITE; PS00108; PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00179; EGF CA; 1.
SMART; SM00001; EGF like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              He Z.H., Cheeseman I., He D., Kohorn B.D.;
"A cluster of five cell wall associated receptor k
are expressed in specific organs of Arabidopsis.";
plant Mol. Biol. 39:1189-1196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; ProDom; PD000001; Euk p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF Ca. I
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY039917; AAK64021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ009696; CAA08794.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99308512; PubMed=10380805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002290;
InterPro; IPR004040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I- SIMILARITY: BELONGS TO THE SER/THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
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                                      46
                                                                                                                                                                                                                                                                                                                                                                       SM00221; STYKC; 1.
                                                                                                              æ
                                                                                                                                                                    Similarity
TMSCKRKEFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ 382
                                                                         CRCNEGFDGNEYLSAGCQDVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT
                                    TNSVK----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                                                            CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR----YCNA----SV 45
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
                                                                                                                                                                  8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ
NGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                pkinasė; 1.
                                                                                                                                                 27;
                                                                                                                                                                  Score 80; E
Pred. No. 8;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                    UNKCNOWN_1.
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                                                                                                                                                                                     DB 10;
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                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases.
OF PROTEIN
                                                                                                                                                                                   Length 735;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes, Wak1-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲
                                                                                                                                                   46;
                                                                                                                                                                                                                                                               Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosidae;
                                                                                                                                                 Gaps
                                      97
                                                                           323
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SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;

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246

98

187

46

127

001892;

001892

R08F11.7 R08F11.7 protein.

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304 124 244 38 R R R R

SEQUENCE FROM N.A. STRAIN-BRISTOL N2;

Minx P.

SEQUENCE FROM N.A. STRAIN=BRISTOL N2;

Query Match Best Local Si Matches 40;

Similarity

40;

184

23

65

86

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RESULT
Q8VFW0
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Q26489
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Best Local S
Matches 39
                                                            QBVFW0;
01-MAR-2002 (TrEMBLrel. 20, Cr.
01-MAR-2002 (TrEMBLrel. 20, La.
01-JUN-2002 (TrEMBLrel. 21, La.
Olfactory receptor MOR202-16.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z68888; CAA93116.1;
HSSP; Q99405; IMPT.
InterPro; IPRO002174; Furin-like.
InterPro; IPRO00209; Peptidase_S8.
InterPro; IPRO00284; P_domain.
Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
SMART; SM00261; FU; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                            Protease.
SEQUENCE
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Prerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.

NCBI TaxID=7108;
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
SEQUENCE FROM N.A.
                                                                                                                                              Q8VFW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and functional characterization of FURIN from frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG-----
                                                                                                                                                                                                                                                                                         TCLGLS-----LIISLAV-----FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN
                                                                                                                                                                                                               --VEYSR----LPRTDVDFTV----LTSCTDQEGPVEYEH
                                                                                                                                                                                                                                                                                                                     CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIAEW
                                                                                                                                                                                                                                                                                                                                              CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W
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                                     Chordata;
Rodentia;
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20, Last sequence up
21, Last annotation
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; Pred. No. 17;
26; Mismatches
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Last annotation update)
                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 15
Q9H677
Search completed: June 23, Job time : 85.0818 secs
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Matches 35
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Best Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKOZG184; BAB15387.1;
SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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"The olfactory receptor gene superfamily Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA: FLJ22531 fis, clone HRC12890.
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01-MAR-2001
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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EMBL, AY073405; AAL61068.1; -
InterPro; IPR000276; GPCR Rhodpsn.
Pfam, PF00001; 7tm 1; 1.
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                                                                                                           289
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                                                                                                           IMGVYTLLTTHLN
                                                                                                                                                            -EGATILVTTKTN 162
                                                                                                                                                                                                                PNLDLNLDR----DLVLP-DVSYQVESSEEDQSQTMDPQGQTLLLFLFVDFHSAFPVQQME
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llarity 26.3%;
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llarity 30.4%;
Conservative 1
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                           2003, 08:39:06
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Pred. No. 4.4;
15; Mismatches
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Shibahara T.,
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